



Notice to Comply

Application No.
09/868,469

Applicant(s)
Benkovic et al.

Examiner
Christian L. Fronda

Art Unit
1652

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set in the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other:

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (571) 272-2510

For CRF Submission Help, call (571) 272-2501/2583.

PatentIn Software Program Support

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

- ☒ **Attachments** Raw Sequence Listing Error Report 03/31/2005.

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

Source:

Date Processed by STIC:

09/868,469
JFW/16
3-31-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses.

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/868,469

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY ITO SOFTWARE

1. Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to J; this will prevent "wrapping."

2. Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3. Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4. Non-ASCII The submitted file was not saved in ASCII(DOS)ical as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5. Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6. PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7. Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
 (1) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
 (11) SEQUENCE OF DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

Please also adjust the "(11) NUMBER OF SEQUENCES" response to include the skipped sequences.

8. Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 <210> sequence id number
 <400> sequence id number
 000

9. Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10. Invalid <211>
Response Per 1.823 of Sequence Rules, the only valid <211> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <211> response is Unknown, Artificial Sequence.

11. Use of <220>

Use of <220> to <223> is MANDATORY if <211> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12. PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13. Misuse of n/Xaa

"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/868,469

DATE: 03/31/2005

TIME: 15:13:49

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03312005\I868469.raw

L:17 M:270 C: Current Application Number differs, Replaced Current Application No
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:301 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:527 SEQ:7
L:301 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11
L:301 M:112 C: (48) String data converted to lower case,
L:301 M:252 E: No. of Seq. differs, <211> LENGTH:Input:522 Found:527 SEQ:7

Best Available Copy



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/868,469

DATE: 03/31/2005

TIME: 15:13:48

Input Set : A:\PTO.SR.txt

Output Set : N:\CRF4\03312005\I868469.raw

5 <110> APPLICANT: THE PENN STATE RESEARCH FOUNDATION
9 <120> TITLE OF INVENTION: Cyclic Peptides
13 <130> FILE REFERENCE: 6460-18
C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/868,469
C--> 17 <141> CURRENT FILING DATE: 2001-09-24
17 <160> NUMBER OF SEQ ID NOS: 7
21 <170> SOFTWARE: PatentIn version 3.0

ERRORED SEQUENCES

Does Not Comply
Corrected Diskette Needed

(pg. 1-2) @

263 <210> SEQ ID NO: 7
265 <211> LENGTH: 522
267 <212> TYPE: DNA
269 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
275 <221> NAME/KEY: misc_feature
277 <223> OTHER INFORMATION: pARCP2-6H
281 <400> SEQUENCE: 7
282 atggttaaag ttatcggtcg tcgttcctc ggagtgcaaa gaatatttga tattggtctt 60
284 cccaagacc ataattttct gctagccaat ggggcgatcg cccacaattg tcatatgcac 120
286 caccaccacc accatggggc aggtgctgca tgcctcagtt ttggcaccga aattttaacc 180
288 gttgagtacg gccattgcc cattggcaaa attgtgagtg aagaaattaa ttgttctgtg 240
290 tacagtgttg atccagaagg gagagtttac acccaggcga tcgccaatg gcatgaccgg 300
292 ggagagcagg aagtattgga atatgaattg gaagatgggt cagtaatccg agctacctct 360
294 gaccaccgct ttttaaccac cgattatcaa ctgttggcga tcgaagaaat ttttgctagg 420
296 caactggact tgttgacttt agaaaatatt aagcaaactg aagaagctct tgacaaccat 480
298 cgttttccct ttccattact tgacgctggg acaattaaat aa 522
E--> 301 (wp213126;1)

pls delete



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Page 2

<210> 3

<211> 14

<212> PRT

<213> Artificial Sequence

What is the source of
Genetic material.

<220>

<221> misc_feature

<223> CHMHGHHHHGAGAA

Invalid
response

See item # 11 on
error summary
sheet.

<400> 3

Cys His Met His His His His His His Gly Ala Gly Ala Ala
1 5 10

The type of errors shown exist throughout
the sequence listing. Please check subsequent
sequences for similar errors.